



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Reetz, Manfred; Zonta, Albin; Schimossek, Klaus; Liebeton, Klaus; Jager, Karl-Erich
- (ii) TITLE OF INVENTION: A Process for the Preparation and Identification of Novel Hydrolases Having Improved Properties
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS
- (A) ADDRESSEE: Norris McLaughlin & Marcus
  - (B) STREET: 220 East 42<sup>nd</sup> Street, 30<sup>th</sup> Floor
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10017
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 09/463,494
  - (B) FILING DATE: 25-JUL-2000
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/EP98/04612
  - (B) FILING DATE: 23-JUL-1998
- (viii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: DE 197 31 990.4
  - (B) FILING DATE: 25-JUL-1997
- (ix) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Briscoe, Kurt G.
  - (B) REGISTRATION NUMBER: 33141
  - (C) REFERENCE/DOCKET NUMBER: STUDIEN 268
- (x) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (212) 808-0700
  - (B) TELEFAX: (212) 808-0844

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GC GCAATTAA CCTCACTAA AGGGAACAAA

30

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGGTAATACG ACTCACTATA GGGCGAA

27

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1049 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION:85..1017

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

B' cont.

GGATCCCCCG GTTCTCCCCG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC	60
CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TAT CTG CTC CCC CTC	111
Met Lys Lys Lys Tyr Leu Leu Pro Leu	
-26 -25 -20	
GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG	159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln	
-15 -10 -5	
GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC	207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly	
1 5 10 15	
ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT	255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile	
20 25 30	
CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC	303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val	
35 40 45	
AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG	351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln	
50 55 60	
GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC	399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile	
65 70 75	

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC GTC GCC GCC GTA CGT	447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg	
80 85 90 95	
CCC GAC CTG ATC GCT TCC GCC ATC AGC GTC GGC GCC CCG CAC AAG GGT	495
Pro Asp Leu Ile Ala Ser Ala Ile Ser Val Gly Ala Pro His Lys Gly	
100 105 110	
TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC	543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly	
115 120 125	
GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC	591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser	
130 135 140	
TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG	639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu	
145 150 155	
GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG	687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro	
160 165 170 175	
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC	735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn	
180 185 190	
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC	783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe	
195 200 205	
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG	831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys	
210 215 220	
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG	879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu	
225 230 235	
GGC ATG GTG ATC CGC GAC AAC TAC CCG ATG AAC CAC CTG GAC GAG GTG	927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val	
240 245 250 255	
AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC	975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser	
260 265 270	
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG	1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu	
275 280 285	
TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC	1049

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Lys Lys Lys Tyr Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala  
 -26 -25 -20 -15  
 Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr  
 -10 -5 1 5  
 Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile  
 10 15 20  
 Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp  
 25 30 35  
 Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu  
 40 45 50  
 Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu  
 55 60 65 70  
 Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro  
 75 80 85  
 Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala  
 90 95 100  
 Ile Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu  
 105 110 115  
 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu  
 120 125 130  
 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr  
 135 140 145 150  
 Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly  
 155 160 165  
 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala  
 170 175 180  
 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp  
 185 190 195  
 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe  
 200 205 210  
 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly  
 215 220 225 230  
 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn  
 235 240 245  
 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr  
 250 255 260

81  
 cont.

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn  
 265 270 275

Arg Leu Lys Asn Ala Ser Leu  
 280 285

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1049 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION:85..1017

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

*b<sup>1</sup>  
unk.*

GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC	60
CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC	111
Met Lys Lys Lys Ser Leu Leu Pro Leu	
-26 -25 -20	
GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG	159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln	
-15 -10 -5	
GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG GCC CAC GGC	207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly	
1 5 10 15	
ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT	255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile	
20 25 30	
CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC	303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val	
35 40 45	
AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG	351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln	
50 55 60	
GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC	399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile	
65 70 75	
GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT	447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg	
80 85 90 95	

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly 100 105 110	495
TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly 115 120 125	543
GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser 130 135 140	591
TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu 145 150 155	639
GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro 160 165 170 175	687
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn 180 185 190	735
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe 195 200 205	783
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys 210 215 220	831
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu 225 230 235	879
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val 240 245 250 255	927
AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser 260 265 270	975
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu 275 280 285	1017
TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC	1049

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala  
 -26 -25 -20 -15  
 Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr  
 -10 -5 1 5  
 Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile  
 10 15 20  
 Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp  
 25 30 35  
 Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu  
 40 45 50  
 Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu  
 55 60 65 70  
 Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro  
 75 80 85  
 Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala  
 90 95 100  
 Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu  
 105 110 115  
 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu  
 120 125 130  
 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr  
 135 140 145 150  
 Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly  
 155 160 165  
 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala  
 170 175 180  
 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp  
 185 190 195  
 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe  
 200 205 210  
 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly  
 215 220 225 230  
 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn  
 235 240 245  
 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr  
 250 255 260  
 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn  
 265 270 275  
 Arg Leu Lys Asn Ala Ser Leu  
 280 285

## (2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1049 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION:85..1017

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC 60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC 111  
 Met Lys Lys Lys Ser Leu Leu Pro Leu  
 -26 -25 -20

B' *cont.* GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG 159  
 Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln  
 -15 -10 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC 207  
 Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly  
 1 5 10 15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT 255  
 Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile  
 20 25 30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC 303  
 Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val  
 35 40 45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG 351  
 Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln  
 50 55 60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC 399  
 Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile  
 65 70 75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT 447  
 Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg  
 80 85 90 95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT 495  
 Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly  
 100 105 110



TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA COG GGT TCG GCC GGC	543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly	
115 120 125	
GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC	591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser	
130 135 140	
TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TTA CTG GGC TCG CTG	639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Leu Leu Gly Ser Leu	
145 150 155	
GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG	687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro	
160 165 170 175	
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC	735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn	
180 185 190	
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC	783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe	
195 200 205	
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG	831
Leu Asp Pro Ser Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys	
210 215 220	
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG	879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu	
225 230 235	
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG	927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val	
240 245 250 255	
AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC	975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser	
260 265 270	
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG	1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu	
275 280 285	
TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC	1049

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala  
 -26 -25 -20 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr  
 -10 -5 1 5  
 Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile  
 10 15 20  
 Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp  
 25 30 35  
 Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu  
 40 45 50  
 Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu  
 55 60 65 70  
 Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro  
 75 80 85  
 Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala  
 90 95 100  
 Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu  
 105 110 115  
 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu  
 120 125 130  
 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr  
 135 140 145 150  
 Gly Thr Gln Asn Leu Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly  
 155 160 165  
 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala  
 170 175 180  
 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp  
 185 190 195  
 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe  
 200 205 210  
 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly  
 215 220 225 230  
 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn  
 235 240 245  
 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr  
 250 255 260  
 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn  
 265 270 275  
 Arg Leu Lys Asn Ala Ser Leu  
 280 285

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1047 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION:84..1016

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION:162..1016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGATCCCCGG TTCTCCCGGA AGGATTCGGG CGATGGCTGG CAGGACGCGC CCCTCGGCC 60

CATCAACCTG AGATGAGAAC AAC ATG AAG AAG AAG TCT CTG CTC CCC CTC 110  
 Met Lys Lys Lys Ser Leu Leu Pro Leu  
 -26 -25 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG 158  
 Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln  
 -15 -10 -5

*B' 60x.* GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC 206  
 Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly  
 1 5 10 15

ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT 254  
 Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile  
 20 25 30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC 302  
 Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val  
 35 40 45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG 350  
 Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln  
 50 55 60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC 398  
 Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile  
 65 70 75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT 446  
 Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg  
 80 85 90 95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT 494  
 Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly  
 100 105 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC 542  
 Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly  
 115 120 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC	590
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser	
130 135 140	
TTC CTT TCC AGC GGC AGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG	638
Phe Leu Ser Ser Gly Ser Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu	
145 150 155	
GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG	686
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro	
160 165 170 175	
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC	734
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn	
180 185 190	
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC	782
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe	
195 200 205	
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG	830
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys	
210 215 220	
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG	878
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu	
225 230 235	
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG	926
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val	
240 245 250 255	
AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC	974
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser	
260 265 270	
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG	1016
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu	
275 280 285	
TAGGACCCCG GCCGGGGCCT CGGCCCGGC C	1047

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala  
 -26 -25 -20 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr  
 -10 -5 1 5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile  
 10 15 20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp  
 25 30 35  
 Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu  
 40 45 50  
 Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu  
 55 60 65 70  
 Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro  
 75 80 85  
 Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala  
 90 95 100  
 Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu  
 105 110 115  
 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu  
 120 125 130  
 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Ser Thr  
 135 140 145 150  
 Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly  
 155 160 165  
 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala  
 170 175 180  
 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp  
 185 190 195  
 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe  
 200 205 210  
 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly  
 215 220 225 230  
 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn  
 235 240 245  
 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr  
 250 255 260  
 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn  
 265 270 275  
 Arg Leu Lys Asn Ala Ser Leu  
 280 285

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1049 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:85..1017

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC 60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC 111  
Met Lys Lys Lys Ser Leu Leu Pro Leu  
-26 -25 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG 159  
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln  
-15 -10 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC 207  
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly  
1 5 10 15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT 255  
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile  
20 25 30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC 303  
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly  
35 40 45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG 351  
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Gln Gln  
50 55 60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC 399  
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile  
65 70 75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT 447  
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg  
80 85 90 95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT 495  
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly  
100 105 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC 543  
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly  
115 120 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC 591  
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser  
130 135 140

TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TTA CTG GGC TCG CTG 639  
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Leu Leu Gly Ser Leu  
145 150 155

B'  
cont.

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro 160 165 170 175	687
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn 180 185 190	735
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe 195 200 205	783
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys 210 215 220	831
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu 225 230 235	879
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val 240 245 250 255	927
AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser 260 265 270	975
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu 275 280 285	1017
TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC	1049

## (2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala  
 -26 -25 -20 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr  
 -10 -5 1 5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile  
 10 15 20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp  
 25 30 35

Gly Ala Gln Val Tyr Val Thr Glu Gly Ser Gln Leu Asp Thr Ser Glu  
 40 45 50

B'  
cont.

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu  
 55 60 65 70  
 Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro  
 75 80 85  
 Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala  
 90 95 100  
 Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu  
 105 110 115  
 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu  
 120 125 130  
 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr  
 135 140 145 150  
 Gly Thr Gln Asn Leu Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly  
 155 160 165  
 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala  
 170 175 180  
 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp  
 185 190 195  
 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe  
 200 205 210  
 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly  
 215 220 225 230  
 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn  
 235 240 245  
 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr  
 250 255 260  
 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn  
 265 270  
 Arg Leu Lys Asn Ala Ser Leu  
 280 285

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 85..1017

(ix) FEATURE:



(A) NAME/KEY: mat\_peptide  
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC 60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC 111  
Met Lys Lys Lys Ser Leu Leu Pro Leu  
-26 -25 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG 159  
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln  
-15 -10 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC 207  
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly  
1 5 10 15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT 255  
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile  
20 25 30

CCC AAC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC 303  
Pro Asn Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly  
35 40 45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG 351  
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Gln Gln  
50 55 60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC 399  
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile  
65 70 75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT 447  
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg  
80 85 90 95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT 495  
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly  
100 105 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC 543  
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly  
115 120 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC 591  
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser  
130 135 140

TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TTA CTG GGC TCG CTG 639  
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Leu Leu Gly Ser Leu  
145 150 155

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG 687  
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro  
160 165 170 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCT TAC AAG GTC AAC	735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn	
180 185 190	
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC	783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe	
195 200 205	
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG	831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys	
210 215 220	
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG	879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu	
225 230 235	
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG	927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val	
240 245 250 255	
AAC CAG GTC CTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC	975
Asn Gln Val Leu Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser	
260 265 270	
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG	1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu	
275 280 285	
TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CCG	1050

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala  
 -26 -25 -20 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr  
 -10 -5 1 5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile  
 10 15 20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Asn Ala Leu Arg Arg Asp  
 25 30 35

Gly Ala Gln Val Tyr Val Thr Glu Gly Ser Gln Leu Asp Thr Ser Glu  
 40 45 50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu  
 55 60 65 70

(2) INFORMATION FOR SEQ ID NO: 15:

(A) LENGTH: 1049 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ix) FEATURE:

- (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION:163..1017

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC 60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG TCT CTG CTC CCC CTC 111  
Met Lys Lys Lys Ser Leu Leu Pro Leu  
-26 -25 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG 159  
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln  
-15 -10 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC 207  
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly  
1 5 10 15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT 255  
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile  
20 25 30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC 303  
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly  
35 40 45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG 351  
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln  
50 55 60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC 399  
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile  
65 70 75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT 447  
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg  
80 85 90 95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AGG GGT 495  
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Arg Gly  
100 105 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC 543  
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly  
115 120 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC 591  
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser  
130 135 140

TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TTA CTG GGC TCG CTG 639  
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Leu Leu Gly Ser Leu  
145 150 155

GAG TCG CTG AAC AGT GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG 687  
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro  
160 165 170 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCT TAC AAG GTC AAC 735  
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn  
180 185 190

B'  
cont.

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC	783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe	
195 200 205	
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG	831
Leu Asp Pro Ser Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys	
210 215 220	
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG	879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu	
225 230 235	
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG	927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val	
240 245 250 255	
AAC CAG GTC CTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC	975
Asn Gln Val Leu Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser	
260 265 270	
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG	1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu	
275 280 285	
TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC	1049

B' *unt.*  
(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala	
-26 -25 -20 -15	
Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr	
-10 -5 1 5	
Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile	
10 15 20	
Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp	
25 30 35	
Gly Ala Gln Val Tyr Val Thr Glu Gly Ser Gln Leu Asp Thr Ser Glu	
40 45 50	
Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu	
55 60 65 70	
Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro	
75 80 85	
Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala	
90 95 100	

Thr Ser Val Gly Ala Pro His Arg Gly Ser Asp Thr Ala Asp Phe Leu  
 105 110 115  
 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu  
 120 125 130  
 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr  
 135 140 145 150  
 Gly Thr Gln Asn Leu Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly  
 155 160 165  
 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala  
 170 175 180  
 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp  
 185 190 195  
 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe  
 200 205 210  
 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly  
 215 220 225 230  
 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn  
 235 240 245  
 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Leu Gly Leu Thr  
 250 255 260  
 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn  
 265 270 275  
 Arg Leu Lys Asn Ala Ser Leu  
 280 285

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 85..1017

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC 60

CCATCAACCT GAGATGAGAA CAAC	ATG AAG AAG AAG TCT CTG CTC CCC CTC	111
	Met Lys Lys Lys Ser Leu Leu Pro Leu	
	-26 -25 -20	
GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG	159	
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln		
-15 -10 -5		
GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC	207	
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly		
1 5 10 15		
ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT	255	
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile		
20 25 30		
CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC	303	
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly		
35 40 45		
AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG	351	
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln		
50 55 60		
GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC	399	
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile		
65 70 75		
GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT	447	
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg		
80 85 90 95		
CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT	495	
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly		
100 105 110		
TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC	543	
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly		
115 120 125		
GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC	591	
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser		
130 135 140		
TTC CTT TCC AGC GGC GGC ATC GGT ACG CAG AAT TTT CTG GGC TCG CTG	639	
Phe Leu Ser Ser Gly Gly Ile Gly Thr Gln Asn Phe Leu Gly Ser Leu		
145 150 155		
GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG	687	
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro		
160 165 170 175		
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC	735	
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn		
180 185 190		
GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC	783	
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe		
195 200 205		

B'  
cont.

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG	831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys	
210 215 220	
AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG	879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu	
225 230 235	
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG	927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val	
240 245 250 255	
AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC	975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser	
260 265 270	
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG	1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu	
275 280 285	
TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC	1049

## (2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala  
 -26 -25 -20 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr  
 -10 -5 1 5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile  
 10 15 20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp  
 25 30 35

Gly Ala Gln Val Tyr Val Thr Glu Gly Ser Gln Leu Asp Thr Ser Glu  
 40 45 50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu  
 55 60 65 70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro  
 75 80 85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala  
 90 95 100

Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu  
 105 110 115



Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu  
 120 125 130  
 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Ile  
 135 140 145 150  
 Gly Thr Gln Asn Phe Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly  
 155 160 165  
 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala  
 170 175 180  
 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp  
 185 190 195  
 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe  
 200 205 210  
 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly  
 215 220 225 230  
 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn  
 235 240 245  
 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr  
 250 255 260  
 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn  
 265 270 275  
 Arg Leu Lys Asn Ala Ser Leu  
 280 285

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGCAATTAA CCCTCACTAA AGGGAACAAA

30

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGTACGCAGA ATNNNCTGGG CTCGC

25

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGTAATACG ACTCACTATA GGGCGAA

27

B'  
cont.